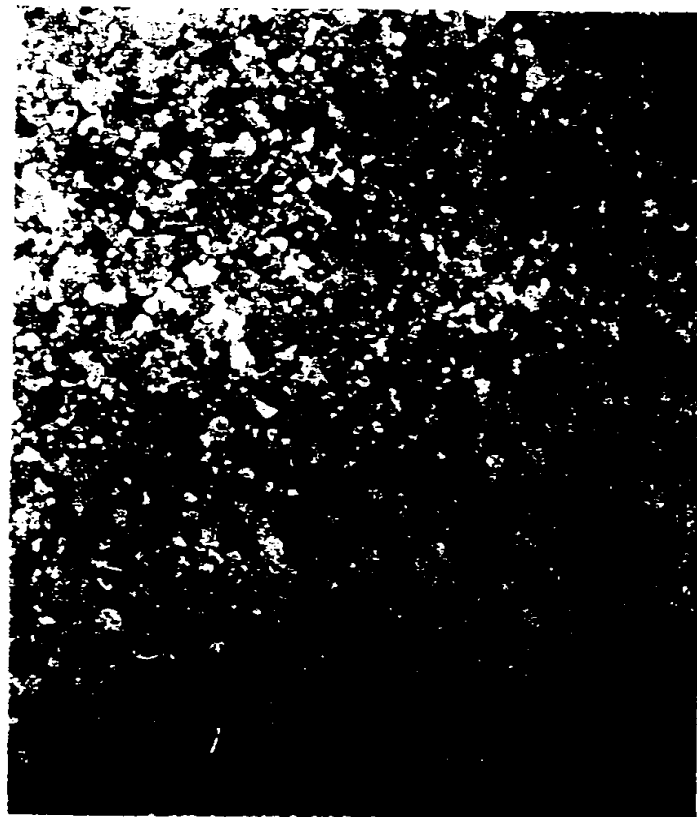


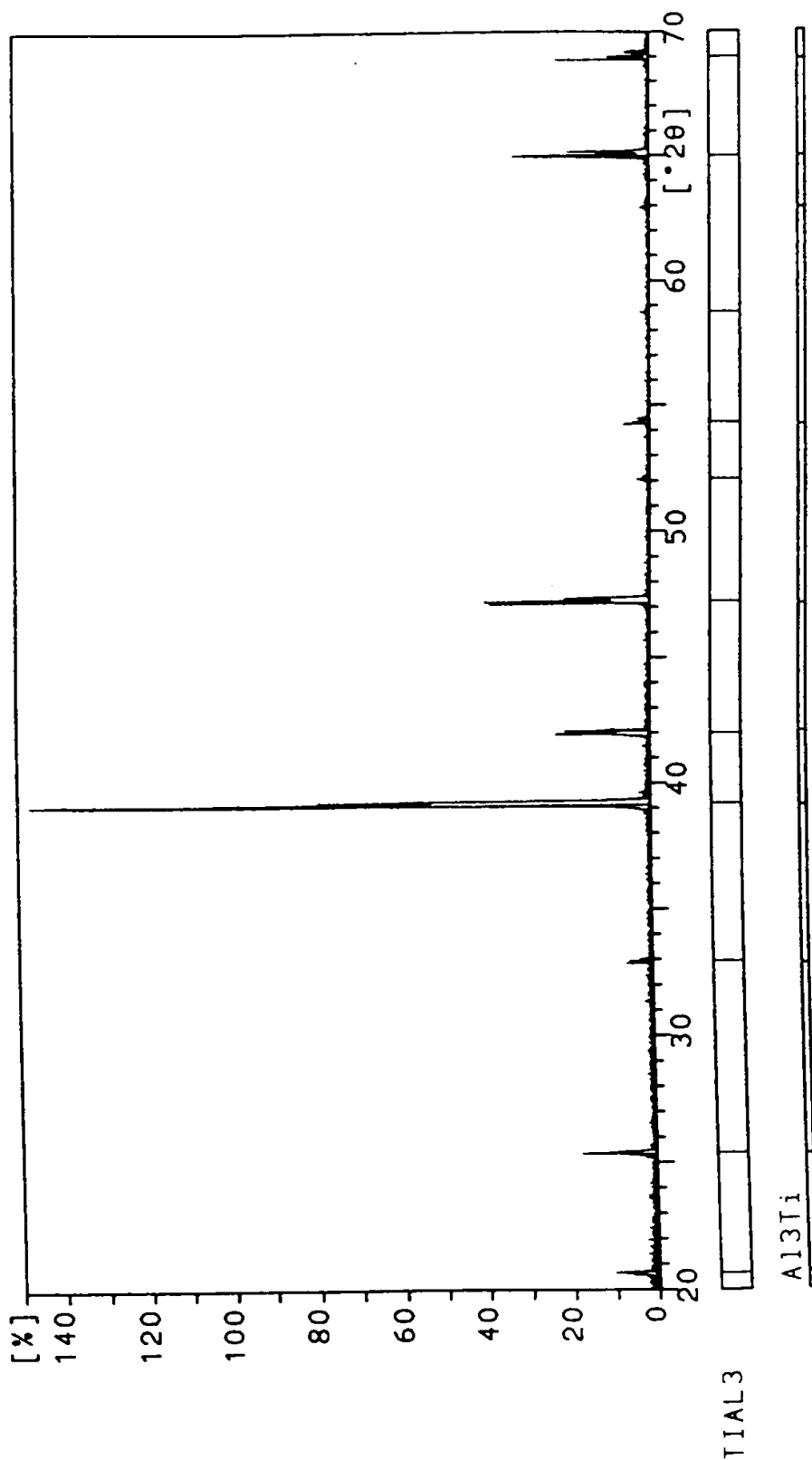
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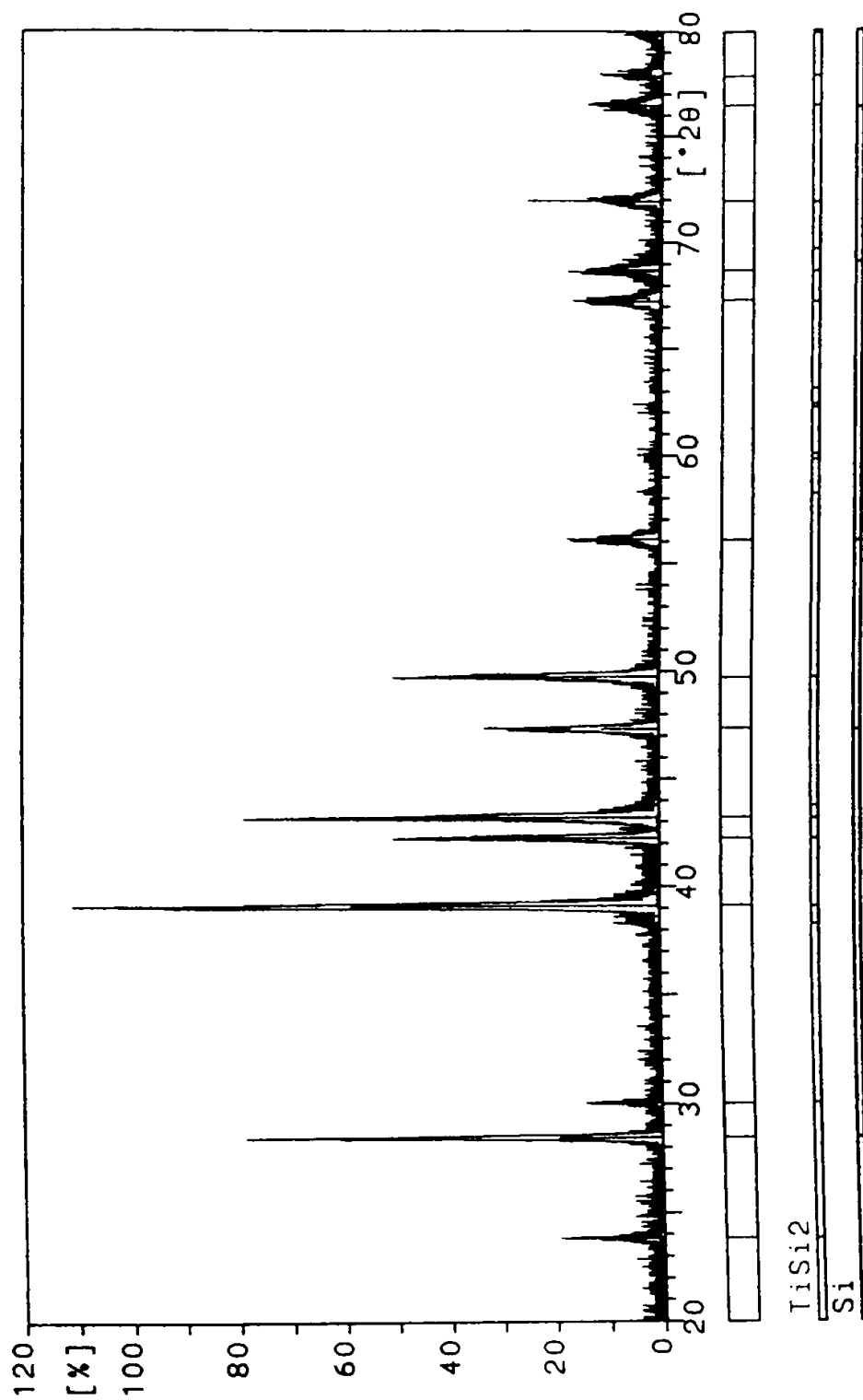
2/6



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1. *Phylogenetic relationships*—Phylogenetic relationships were determined using the maximum parsimony method. The analysis was performed using the program PAUP 4.0 (Nelson & OlSEN, 1992). The analysis was based on 1000 random addition sequence replicates and 1000 random addition sequence replicates. The analysis was based on 1000 random addition sequence replicates and 1000 random addition sequence replicates. The analysis was based on 1000 random addition sequence replicates and 1000 random addition sequence replicates.

3/6



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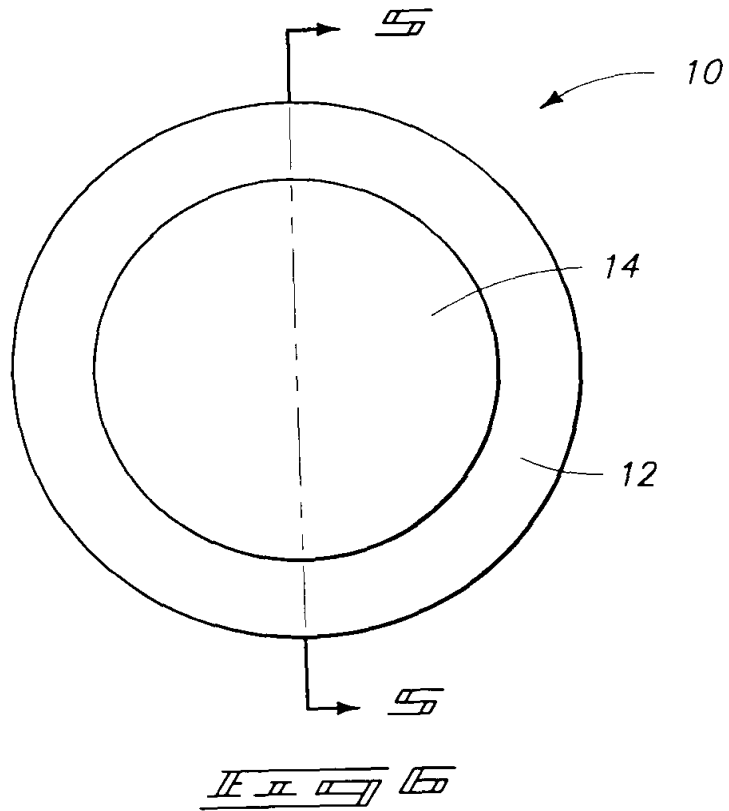
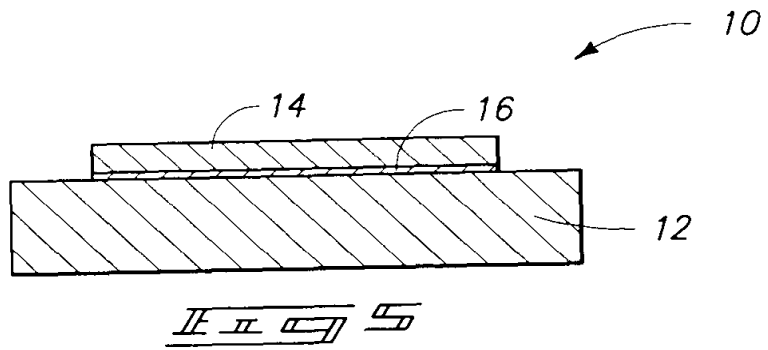
4/6



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5/6



6/6

